

OIEP

RAW SEQUENCE LISTING
 PATENT APPLICATION: US/09/904,568

DATE: 07/26/2001
 TIME: 18:43:12

Input Set : A:\1272591.app
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ENTERED

3 <110> APPLICANT: TREMBLAY, Johanne
 4 HAMET, Pavel
 5 LEWANCZUK, Richard
 6 GOSSARD, Francis
 8 <120> TITLE OF INVENTION: A Novel Hypertension Related Calcium Regulated Gene
 9 (HCARG)
 11 <130> FILE REFERENCE: 12725.9
 13 <140> CURRENT APPLICATION NUMBER: US/09/904,568
 14 <141> CURRENT FILING DATE: 2001-07-16
 16 <160> NUMBER OF SEQ ID NOS: 4
 18 <170> SOFTWARE: PatentIn Ver. 2.1
 20 <210> SEQ ID NO: 1
 21 <211> LENGTH: 1100
 22 <212> TYPE: DNA
 23 <213> ORGANISM: Rattus rattus
 25 <220> FEATURE:
 26 <221> NAME/KEY: CDS
 27 <222> LOCATION: (132)..(803)
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 32 ttggtttgta ttgtaatgc aactgtggtt aggaccttct ctctcgactg gtcaagaaac 120
 34 ggaagaagaag g/atg tct gct ttg ggg gct gca gct cca tac ttg cac cat 170
 35 Met Ser Ala Leu Gly Ala Ala Ala Pro Tyr Leu His His
 36 1 5 10
 38 ccc gct gac agt cac agt ggc cgg gtc agt ttc ctg ggt tcc cag ccc 218
 39 Pro Ala Asp Ser His Ser Gly Arg Val Ser Phe Leu Gly Ser Gln Pro
 40 15 20 25
 42 tct cca gaa gtg acg gcc gtg gct cag ctc ttg aag gac tta gac agg 266
 43 Ser Pro Glu Val Thr Ala Val Ala Gln Leu Leu Lys Asp Leu Asp Arg
 44 30 35 40 45
 46 agc acc ttc aga aag ttg ttg aaa ctt gta gtc ggg gcc ctg cat ggg 314
 47 Ser Thr Phe Arg Lys Leu Leu Lys Leu Val Val Gly Ala Leu His Gly
 48 50 55 60
 50 aaa gac tgc aga gaa gct gtg gag caa ctt ggt gcc agc gcc aac ctg 362
 51 Lys Asp Cys Arg Glu Ala Val Glu Gln Leu Gly Ala Ser Ala Asn Leu
 52 65 70 75
 54 tca gaa gag cgt ctg gcc gtc ctg ctg gcg ggc aca cac acc ctg ctc 410
 55 Ser Glu Glu Arg Leu Ala Val Leu Leu Ala Gly Thr His Thr Leu Leu
 56 80 85 90
 58 cag cag gct ctc cgg ctg ccc cct gct agt cta aag cca gat gcc ttc 458
 59 Gln Gln Ala Leu Arg Leu Pro Pro Ala Ser Leu Lys Pro Asp Ala Phe
 60 95 100 105
 62 cag gaa gag ctc cag gaa ctt ggc att cct cag gat cta att gga gat 506
 63 Gln Glu Glu Leu Gln Glu Leu Gly Ile Pro Gln Asp Leu Ile Gly Asp
 64 110 115 120 125
 66 ttg gcc agt ttg gca ttt ggg agt caa cgc cct ctt ctc gac tct gta 554
 67 Leu Ala Ser Leu Ala Phe Gly Ser Gln Arg Pro Leu Leu Asp Ser Val

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70 gcc caa cag cag gga tcc tgc ctg cct cac gtg tct tac ttc cgg tgg 602
71 Ala Gln Gln Gln Gly Ser Ser Leu Pro His Val Ser Tyr Phe Arg Trp
72                               145                               155
74 cgg gtg gac gtg gcc atc tca acc agc gct cag tcc cgc tcc ctg caa 650
75 Arg Val Asp Val Ala Ile Ser Thr Ser Ala Gln Ser Arg Ser Leu Gln
76                               160                               170
78 ccg agt gtt ctc atg cag ctg aag ctc aca gat gga tct gca cac cgc 698
79 Pro Ser Val Leu Met Gln Leu Lys Leu Thr Asp Gly Ser Ala His Arg
80                               175                               185
82 ttc gag gtg ccc ata gcc aaa ttt cag gag ctg cgg tac agt gta gcc 746
83 Phe Glu Val Pro Ile Ala Lys Phe Gln Glu Leu Arg Tyr Ser Val Ala
84 190                               195                               200
86 ttg gtc ctt aag gag atg gca gaa ctg gag aag aag tgt gag cgc aaa 794
87 Leu Val Leu Lys Glu Met Ala Glu Leu Lys Lys Lys Cys Glu Arg Lys
88                               210                               215
90 ctg cag gac tgactgaacc ctgtactgt ggggtctgaa gctggtacca 843
91 Leu Gln Asp
93 gaacacagcc cccactggt gatgagccca actccattga ggtccctgcat gtgagaacgt 903
95 attttaagtg aaaagacagc gggactttca ggttttgttt tatgagtaaa cagctgggca 963
97 ggggtggcaca gttataatc tcagcccttg gaagtctgag gctggagaaat gggaagtga 1023
99 agctgggcct ggttttcca gtgaggctca gtgtcgaatt aaagaggtaa agcaactatt 1083
101 aaaaaaaaaa aaaaaaa
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106 <212> TYPE: PRT
107 <213> ORGANISM: Rattus rattus
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114 20 25 30
116 Val Thr Ala Val Ala Gln Leu Leu Lys Asp Leu Asp Arg Ser Thr Phe
117 35 40 45
119 Arg Lys Leu Leu Lys Leu Val Val Gly Ala Leu His Gly Lys Asp Cys
120 50 55 60
122 Arg Glu Ala Val Glu Gln Leu Gly Ala Ser Ala Asn Leu Ser Glu Glu
123 65 70 75 80
125 Arg Leu Ala Val Leu Leu Ala Gly Thr His Thr Leu Leu Gln Gln Ala
126 85 90 95
128 Leu Arg Leu Pro Pro Ala Ser Leu Lys Pro Asp Ala Phe Gln Glu Glu
129 100 105 110
131 Leu Gln Glu Leu Gly Ile Pro Gln Asp Leu Ile Gly Asp Leu Ala Ser
132 115 120 125
134 Leu Ala Phe Gly Ser Gln Arg Pro Leu Leu Asp Ser Val Ala Gln Gln
135 130 135 140
137 Gln Gly Ser Ser Leu Pro His Val Ser Tyr Phe Arg Trp Arg Val Asp
138 145 150 155 160
140 Val Ala Ile Ser Thr Ser Ala Gln Ser Arg Ser Leu Gln Pro Ser Val

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141                                     165                                     170                                     175
143 Leu Met Gln Leu Lys Leu Thr Asp Gly Ser Ala His Arg Phe Glu Val
144                                     180                                     185                                     190
146 Pro Ile Ala Lys Phe Gln Glu Leu Arg Tyr Ser Val Ala Leu Val Leu
147                                     195                                     200                                     205
149 Lys Glu Met Ala Glu Leu Glu Lys Lys Cys Glu Arg Lys Leu Gln Asp
150                                     210                                     215                                     220
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155 <211> LENGTH: 1355
156 <212> TYPE: DNA
157 <213> ORGANISM: Homo sapiens
159 <220> FEATURE:
160 <221> NAME/KEY: CDS
161 <222> LOCATION: (295)..(966)
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168 gtccacacgg gacagggacg cccgctcgcc tcgctccgc gctgatctcc aaggtctcgc 180
170 ggtttccccc ccgccacccc ggacgcccgc gaaagccagc gagctctcca gctcaggcca 240
172 tctgcatctg ggaccgaact cctgggctgg ctgatcaaa aggaagcagc agcaatg 297
173                                     Met
174                                     1
176 tct gct gtg ggg gct gca act cca tac ctg cat cat cct ggt gat agt 345
177 Ser Ala Val Gly Ala Ala Thr Pro Tyr Leu His His Pro Gly Asp Ser
178                                     5                                     10                                     15
180 cac agt ggc cga gtg agt ttc ttg ggg gcc cag ctt cct cca gag gtg 393
181 His Ser Gly Arg Val Ser Phe Leu Gly Ala Gln Leu Pro Pro Glu Val
182                                     20                                     25                                     30
184 gca gca atg gcc cgg cta cta ggg gac cta gac agg agc acg ttc aga 441
185 Ala Ala Met Ala Arg Leu Leu Gly Asp Leu Asp Arg Ser Thr Phe Arg
186                                     35                                     40                                     45
188 aag ttg ctg aag ttt gtg gtc agc agc ctg cag ggg gag gac tgc cga 489
189 Lys Leu Leu Lys Phe Val Val Ser Ser Leu Gln Gly Glu Asp Cys Arg
190 50                                     55                                     60                                     65
192 gac ggt gtg cag cgt ctt ggg gtc agc gcc aac ctg ccg gag gag cag 537
193 Asp Gly Val Gln Arg Leu Gly Val Ser Ala Asn Leu Pro Glu Glu Gln
194                                     70                                     75                                     80
196 ctg ggt gcc ctg ctg gca ggc atg cac aca ctg ctc cag cag gcc ctc 585
197 Leu Gly Ala Leu Leu Ala Gly Met His Thr Leu Leu Gln Gln Ala Leu
198                                     85                                     90                                     95
199 cgt ctg ccc ccc acc agc ctg aag cct gac acc ttc agg gac cag ctc 633
200 Arg Leu Pro Pro Thr Ser Leu Lys Pro Asp Thr Phe Arg Asp Gln Leu
201                                     100                                     105                                     110
202 cag gag ctc tgc atc ccc caa gac ctg gtc ggg gac ttg gcc agc gtg 681
203 Gln Glu Leu Cys Ile Pro Gln Asp Leu Val Gly Asp Leu Ala Ser Val
204                                     115                                     120                                     125
205 gta ttt ggg agc cag cgg ccc ctc ctt gat tct gtg gcc cag cag cag 729
206                                     130                                     135                                     140                                     145
208 gta ttt ggg agc cag cgg ccc ctc ctt gat tct gtg gcc cag cag cag
209 Val Phe Gly Ser Gln Arg Pro Leu Leu Asp Ser Val Ala Gln Gln Gln
210 130

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212 ggg gcc tgg ctg ccg cat gtt gct gac ttt cgg tgg cgg gtg gat gta 777
213 gly ala trp leu pro his val ala asp phe arg trp arg val asp val
214 150 155 160
216 gca atc tcc acc agt gcc ctg gct cgc tcc ctg cag ccg agc gtc ctg 825
217 ala ile ser thr ser ala leu ala arg ser leu gln pro ser val leu
218 165 170 175
220 atg cag ctg aag ctt tca gat ggg tca gca tac cgc ttt gag gtc ccc 873
221 met gln leu lys leu ser asp gly ser ala tyr arg phe glu val pro
222 180 185 190
224 aca gcc aag ttc cag gag ctg cgg tac agc gtg gcc ctg gtc cta aag 921
225 thr ala lys phe gln glu leu arg tyr ser val ala leu val leu lys
226 195 200 205
228 gag atg gca gat ctg gag aag agg tgt gag cgc aga ctg cag gac 966
229 glu met ala asp leu glu lys arg cys glu arg leu gln asp
230 210 215 220
232 tgaccctcca cttgaccagt cccattcaga tccggtttgg acaggcacct gagatggtgc 1026
234 caaagtgcag ctgactcttc ccacgacagc cctggccttc ccatcaggca ggctcttcag 1086
236 tgagtgtttg aacgtaatta ttagtatttc ttttaattg aaaaagagag ctatgccttt 1146
238 ttttcttttt ggaagtaaag cagctaaaac atgtttctat aggtgagtgt tggaccttca 1206
240 cactccctcc tccctgtaca tttgtctttg gtgctggaag tggccatgtg aggccaggtt 1266
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244 gtagatcttg ttttccaggc agggcccg
247 <210> SEQ ID NO: 4
248 <211> LENGTH: 224
249 <212> TYPE: PRT
250 <213> ORGANISM: Homo sapiens
252 <400> SEQUENCE: 4
253 Met Ser Ala Val Gly Ala Ala Thr Pro Tyr Leu His His Pro Gly Asp
254 1 5 10 15
256 Ser His Ser Gly Arg Val Ser Phe Leu Gly Ala Gln Leu Pro Pro Glu
257 20 25 30
259 Val Ala Ala Met Ala Arg Leu Leu Gly Asp Leu Asp Arg Ser Thr Phe
260 35 40 45
262 Arg Lys Leu Leu Lys Phe Val Val Ser Ser Leu Gln Gly Glu Asp Cys
263 50 55 60
265 Arg Asp Gly Val Gln Arg Leu Gly Val Ser Ala Asn Leu Pro Glu Glu
266 65 70 75 80
268 Gln Leu Gly Ala Leu Ala Gly Met His Thr Leu Leu Gln Gln Ala
269 85 90 95
271 Leu Arg Leu Pro Pro Thr Ser Leu Lys Pro Asp Thr Phe Arg Asp Gln
272 100 105 110
274 Leu Gln Glu Leu Cys Ile Pro Gln Asp Leu Val Gly Asp Leu Ala Ser
275 115 120 125
277 Val Val Phe Gly Ser Gln Arg Pro Leu Leu Asp Ser Val Ala Gln Gln
278 130 135 140
280 Gln Gly Ala Trp Leu Pro His Val Ala Asp Phe Arg Trp Arg Val Asp
281 145 150 155 160
283 Val Ala Ile Ser Thr Ser Ala Leu Ala Arg Ser Leu Gln Pro Ser Val
284 165 170 175

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286	Leu	Met	Gln	Leu	Lys	Leu	Ser	Asp	Gly	Ser	Ala	Tyr	Arg	Phe	Glu	Val
287				180					185						190	
289	Pro	Thr	Ala	Lys	Phe	Gln	Glu	Leu	Arg	Tyr	Ser	Val	Ala	Leu	Val	Leu
290			195					200					205			
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293		210					215					220				

VERIFICATION SUMMARY

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